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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK049639
2514 bp mRNA linear HTC 03-APR-2004 Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:5530010015 product:GLYPICAN-2 PRECURSOR (CEREBROGLYCAN) (HSPG M13) homolog [Rattus norvegicus], full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matamoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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CB182208 AGENCOURT
B0884741 AGENCOURT
CN347353 170006000
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Sciurognathi, Muridae, Murinae, Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK049639
AK049639.1 GI:26340377
HTC; CAP trapper.
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/mol_type="unassigned DNA"
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AX096281 Homo sapi
BC027972 Homo sapi
AL634418 Homo sapi
AX600207 Sequence
AX661921 Sequence
LZ0468 Rattus norv
AX661919 Sequence
AX661919 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AX661919 Sequence
AX093588 Homo sapi
AX661923 Sequence
AF105268 Mus muscu
BD018231 Novel gen
                                                                            November 21, 2004, 18:53:50; Search time 5046 Seconds (without alignments)
16728.520 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX661917 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel
Novel
                                                                                                                           US-10-055-569A(19)
1785
1 atgtccgcgctgcgacctct.....aagggttcatggcccttcc 1785
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                                                                                                                                                                                                                                    9053458
            GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                             4526729 segs, 23644849745 residues
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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RATCRBGLVC
                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                       first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC027972
HSM805505
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AY093588
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AK096281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD018231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BD018230
                                                                                                                                                                         IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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9b_ero: *

9b_ero: *
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99.6 2528
99.6 2528
99.5 2566
99.7 3 2133
81.4 1613
63.8 1976
40.9 2135
19.1 3515
18.8 816
18.8 816
18.6 812
18.6 812
18.1 13764
18.1 18.2 13764
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Gaps

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GCCCGGGGATATAGCTTAAACCTAATCCCTCCCGCCCTGATCTCAGGTGAGCACCTCCGG 180

121 121

셤 8

Homo sapi Homo sapi Sequence

BD098168 N AC073842 H AC092483 H AX937190 S

AC073842 AC092483 AX937190

332.4 325.6 325.6 323

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BD098168

1453.4 1231.8 1139.4 730.4 358.8

1775.4

Score

Result No.

Nove]

GCCGGGGATATAGCTTAAACCTAATCCCTCCGGCCTGATCTCAGGTGAGCACCTCCGG

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November 21, 2004, 18:47:40; Search time 601 Seconds (without alignments)
15591.043 Million cell updates/sec
                                                                                                                                                                                                                     1 atgtccgcgctgcgacctct.....aagggttcatggccctttcc 1785
                                                                                                                                                                                                                                                                                                                                                  8269772
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   4134886 segs, 2624710521 residues
                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 1.0
                                                                                                                                                                  US-10-055-569A(19
                                                                                                                                                                                                                                                            IDENTITY NUC
                                                                                                                                                                                                   Perfect score:
Sequence:
                                                                                                                                                                                                                                                          Scoring table:
                                                                      OM nucleic
                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                         Run on:
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seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries N_Geneseq_233ep04:* Database

genesequib80s:* genesequ200s:* genesequ2000s:* genesequ2001as:* genesequ2001bs:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2003as:* geneseqn2003bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Abs78649 Human CDN Add49106 Human NOV Add49098 Human NOV Add4909 Human NOV Add49104 Human NOV Abs51686 DNA encod Add49092 Human NOV Add49092 Human NOV Add49109 Human NOV Add49109 Human NOV Add49096 Human NOV Add49096 Human NOV Abz5274 Human GPC Abz71193 Novel hum Aby71193 Novel hum Abs51684 DNA encod Add49088 Human NOV Adm02499 Human cDN Abz59273 Human GPC Aah30728 Human col Abs51687 DNA encod Description SUMMARIES ADD49098 ADD49090 ADD49104 ADD49106 ADD49086 ADD49094 ADD49096 ABZ59274 ABZ59273 AAH30728 ABS51687 ABS51686 ABS51684 2 2 2220 22 Query Match Length DB 100.0 100.0 99.6 97.0 97.0 90.8 88.3 81.4 81.4 63.8 63.8 1139.4 1124.6 1101.2 783.4 730.4 485.4 373.8 358.8 Score 1737.4 1730.6 1730.6 1621.4 1575.6 1453.4 1133.4 Result

Add49102 Human NOV	Aai94394 Human neu	Aai94393 Human neu	Aad08307 Human sec	Aad08284 Human sec	Aad54707 Human gly	Adf53593 Haematopo	Ado07726 Human pol	Aaz00685 Human GPC	Abx76377 Lung canc	Abz59272 Human GPC	Acc72657 Human qly	Adn39701 Cancer/an		Add19916 Human sof	Abz59283 Human GPC	Aaz33983 Human PRO	Aac78482 Human PRO	Aas45972 Human DNA		Aca89422 cDNA enco	Aca73432 Human sec	Aca05747 Human sec	
ADD49102 ADO07731	AA194394	AAI94393	AAD08307	AAD08284	AAD54707	ADF53593	AD007726	AAZ00685	ABX76377	ABZ59272	ACC72657	ADN39701	ADN38929	ADQ19916	ABZ59283	AAZ33983	AAC78482	AAS45972	ACA63551	ACA89422	ACA73432	ACA05747	
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20.1	18.8	18.6	18.3	18.3	18.1	18.1	18.1	18.1	18.1	18.1	18.1	18.1	18.1	18.1	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	
358.8	334.8	332.4	326	326	323	323	323	323	323	323	323	323	323	323	318.2	318.2	318.2	318.2	318.2	318.2	318.2	318.2	
23	C 24	. 52	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

Human; NOVX; pathological condition; NOVX-associated disorder;
Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
renal artery stenosis; interstitial nephritis; glomerulonephritis;
polycystic kidney disease; cataract; Alzheimer's disease; cancer;
acoustic trauma; cardiomyopathy; atherosclerosis; hypertenston;
congenital heart defect; scleroderma; endometriosis; haemophilia;
dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;
multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;
ence; wound; askhma; human disease; calpain; epsin; zinc finger;
low density lipoprotein B; LDLB; purinoceptor; CG8841; synaptotagmin;
serine protease TLSP; mitogen activated protein kinase kinase-2;
glypican-2 precursor; thymosin beta-10; gene; ds. DNA encoding human Glypican-2 Precursor-like protein #1. ABS51684 standard; DNA; 1785 BP (first entry) 05-NOV-2002 ABS51684

W0200255702=N3. Com Homo sapiens

18-JUL-2002

26-OCT-2000; 2000US-0243522P. 26-OCT-2000; 2000US-0243642P. 27-OCT-2000; 2000US-024361P. 27-OCT-2000; 2000US-0244443P. 31-OCT-2000; 2000US-0244443P. 01-NOV-2000; 2000US-024495P. 26-00T-2001; 2001WO-US050925 26-OCT-2000;

2000US-0244443P. 2000US-0244995P. 2000US-0245029P. 2000US-0245293P. 2000US-0245315P.

2001US-0262994P